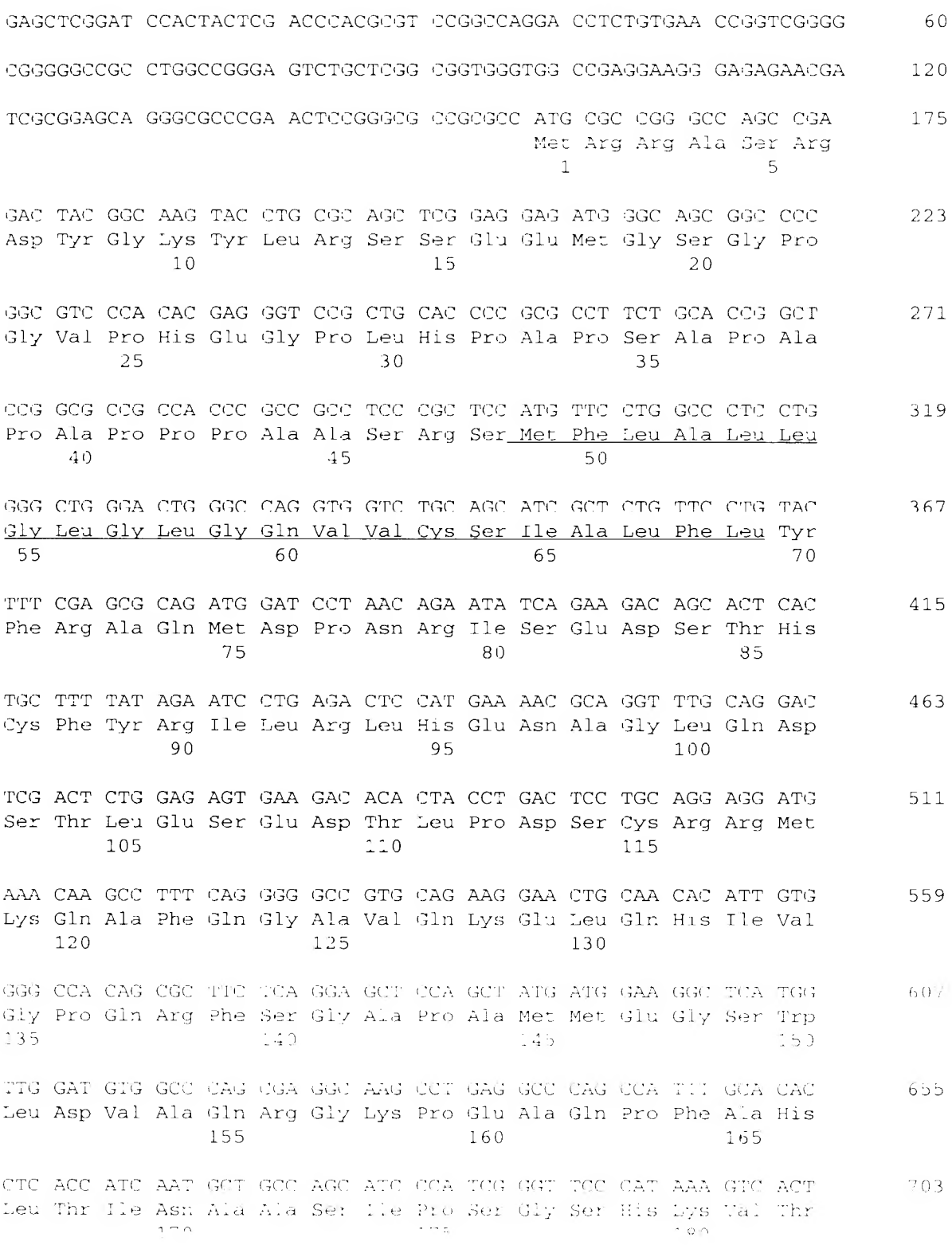
FIGURE 1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CGGGGGCCGC CTGGCCGGGA GTCTGCTCGG CGGTGGGTGG CCGAGGAAGG GAGAGAACGA 120
TCGCGGAGCA GGGCGCCCGA ACTCCGGGCG CCGCGCC ATG CGC CGG GCC AGC CGA 175
Met Arg Arg Ala Ser Arg
1 5
GAC TAC GGC AAG TAC CTG CGC AGC TCG GAG GAG ATG GGC AGC GGC CCC 223
Asp Tyr Gly Lys Tyr Leu Arg Ser Ser Glu Glu Met Gly Ser Gly Pro
10 15 20
GGC GTC CCA CAC GAG GGT CCG CTG CAC CCC GCG CCT TCT GCA CCG GCT 271
Gly Val Pro His Glu Gly Pro Leu His Pro Ala Pro Ser Ala Pro Ala
25 30 35
CCG GCG CCG CCA CCC GCC GCC TCC CGC TCC ATG TTC CTG GCC CTC CTG 319
Pro Ala Pro Pro Pro Ala Ala Ser Arg Ser Met Phe Leu Ala Leu Leu
40 45 50
GGG CTG GGA CTG GGC CAG GTG GTC TGC AGC ATC GCT CTG TTC CTG TAC 367
Gly Leu Gly Leu Gly Gln Val Val Cys Ser Ile Ala Leu Phe Leu Tyr
55 60 65 70
TTT CGA GCG CAG ATG GAT CCT AAC AGA ATA TCA GAA GAC AGC ACT CAC 415
Phe Arg Ala Gln Met Asp Pro Asn Arg Ile Ser Glu Asp Ser Thr His
75 80 85
TGC TTT TAT AGA ATC CTG AGA CTC CAT GAA AAC GCA GGT TTG CAG GAC 463
Cys Phe Tyr Arg Ile Leu Arg Leu His Glu Asn Ala Gly Leu Gln Asp
90 95 100
TCG ACT CTG GAG AGT GAA GAC ACA CTA CCT GAC TCC TGC AGG AGG ATG 511
Ser Thr Leu Glu Ser Glu Asp Thr Leu Pro Asp Ser Cys Arg Arg Met
105 110 115
AAA CAA GCC TTT CAG GGG GCC GTG CAG AAG GAA CTG CAA CAC ATT GTG 559
Lys Gln Ala Phe Gln Gly Ala Val Gln Lys Glu Leu Gln His Ile Val
120 125 130
GGG CCA CAG CGC TTC TCA GGA GCT CCA GCT ATG ATG GAA GGC TCA TGG 607
Gly Pro Gln Arg Phe Ser Gly Ala Pro Ala Met Met Glu Gly Ser Trp
135 140 145 150
TTG GAT GTG GCC CAG CGA GGC AAG CCT GAG GCC CAG CCA TTT GCA CAC 655
Leu Asp Val Ala Gln Arg Gly Lys Pro Glu Ala Gln Pro Phe Ala His
155 160 165
CTC ACC ATC AAT GCT GCC AGC ATC CCA TCG GGT TCC CAT AAA GTC ACT 703
Leu Thr Ile Asn Ala Ala Ser Ile Pro Ser Gly Ser His Lys Val Thr
170 175 180

FIGURE 1 (Con't)

```
ACG TTA AGC AAC GGA AAA CTA AGG GTT AAC CAA GAT GGC TTC TAT TAC          799
Thr Leu Ser Asn Gly Lys Leu Arg Val Asn Gln Asp Gly Phe Tyr Tyr
    200                 205                 210

CTG TAC GCC AAC ATT TGC TTT CGG CAT CAT GAA ACA TCC GGA AGC GTA          847
Leu Tyr Ala Asn Ile Cys Phe Arg His His Glu Thr Ser Gly Ser Val
215                 220                 225                 230

CCT ACA GAC TAT CTT CAG CTG ATG GTG TAT GTC GTT AAA ACC AGC ATC          895
Pro Thr Asp Tyr Leu Gln Leu Met Val Tyr Val Val Lys Thr Ser Ile
                235                 240                 245

AAA ATC CCA AGT TCT CAT AAC CTG ATG AAA GGA GGG AGC ACG AAA AAC          943
Lys Ile Pro Ser Ser His Asn Leu Met Lys Gly Gly Ser Thr Lys Asn
            250                 255                 260

TGG TCG GGC AAT TCT GAA TTC CAC TTT TAT TCC ATA AAT GTT GGG GGA          991
Trp Ser Gly Asn Ser Glu Phe His Phe Tyr Ser Ile Asn Val Gly Gly
        265                 270                 275

TTT TTC AAG CTC CGA GCT GGT GAA GAA ATT AGC ATT CAG GTG TCC AAC         1039
Phe Phe Lys Leu Arg Ala Gly Glu Glu Ile Ser Ile Gln Val Ser Asn
    280                 285                 290

CCT TCC CTG CTG GAT CCG GAT CAA GAT GCG ACG TAC TTT GGG GCT TTC         1087
Pro Ser Leu Leu Asp Pro Asp Gln Asp Ala Thr Tyr Phe Gly Ala Phe
295                 300                 305                 310

AAA GTT CAG GAC ATA GAC T GAGACTCATT TCGTGGAACA TTAGCATGGA               1136
Lys Val Gln Asp Ile Asp
                315

TGTCCTAGAT GTTTGGAAAC TTCTTAAAAA ATGGATGATG TCTATACATG TGTAAGACTA        1196

CTAAGAGACA TGGCCCACGG TGTATGAAAC TCACAGCCCT CTCTCTTGAG CCTGTACAGG        1256

TTGTGTATAT GTAAAGTCCA TAGGTGATGT TAGATTCATG GTGATTACAC AACGGTTTTA        1316

CAATTTTGTA ATGATTTCCT AGAATTGAAC CAGATTGGGA GAGGTATTCC GATGCTTATG        1376

AAAAACTTAC ACGTGAGCTA TGGAAGGGGG TCACAGTCTC TGGGTCTAAC CCCTGGACAT        1436

GTGCCACTGA GAACTTTGAA ATAAAGAGGA TGCCATGTCA TTGCAAAGAA ATGATAGTGT        1496

GAAGGGTTAA GTTCTTTTGA ATTGTTACAT TGCGCTGGGA CCTGCAAATA AGTTCTTTTT        1556

TTCTAATGAG GAGAGAAAAA TATATGTATT TTTATATAAT GTCTAAAGTT ATATTTCAGG        1616

TGTAATGTTT TCTGTGCAAA GTTTTGTAAA TTATATTTGT GCTATAGTAT TTGATTCAAA        1676
```

FIGURE 1 (Con't)

TCAAAACTAT GCAAGCAAAA TAAATAAATA AAAATAAAAT GAATACCTTG AATAATAAGT 1916

AGGATGTTGG TCACCAGGTG CCTTTCAAAT TTAGAAGCTA ATTGACTTTA GGAGCTGACA 1976

TAGCCAAAAA GGATACATAA TAGGCTACTG AAATCTGTCA GGAGTATTTA TGCAATTATT 2036

GAACAGGTGT CTTTTTTTAC AAGAGCTACA AATTGTAAAT TTTGTTTCTT TTTTTTCCCA 2096

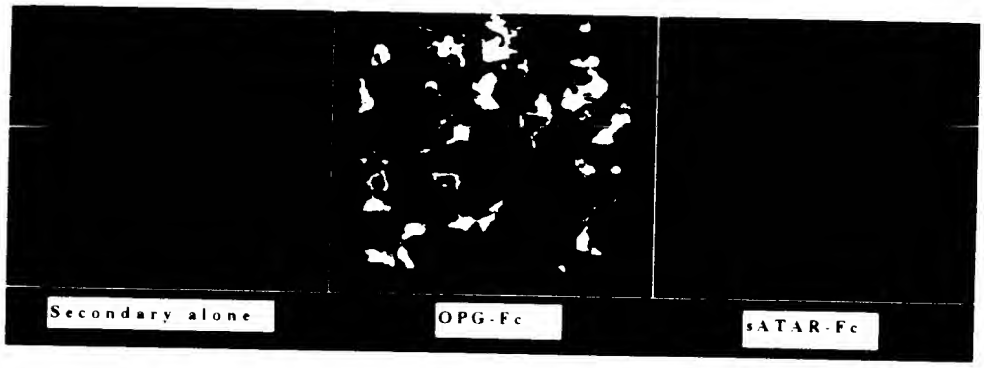
TAGAAAATGT ACTATAGTTT ATCAGCCAAA AAACAATCCA CTTTTTAATT TAGTGAAAGT 2156

TATTTTATTA TACTGTACAA TAAAAGCATT GTCTCTGAAT GTTAATTTTT TGGTACAAAA 2216

AATAAATTTG TACGAAAACC TGAAAAAAAA AAAAAAAAAA AAAAAAAGGG CGGCCGCTCT 2276

AGAGGGCCCT ATTCTATAG 2295

Expression of 32D-F3 in COS-7 Cells



OPG Binding Protein Expression in Human Tissues

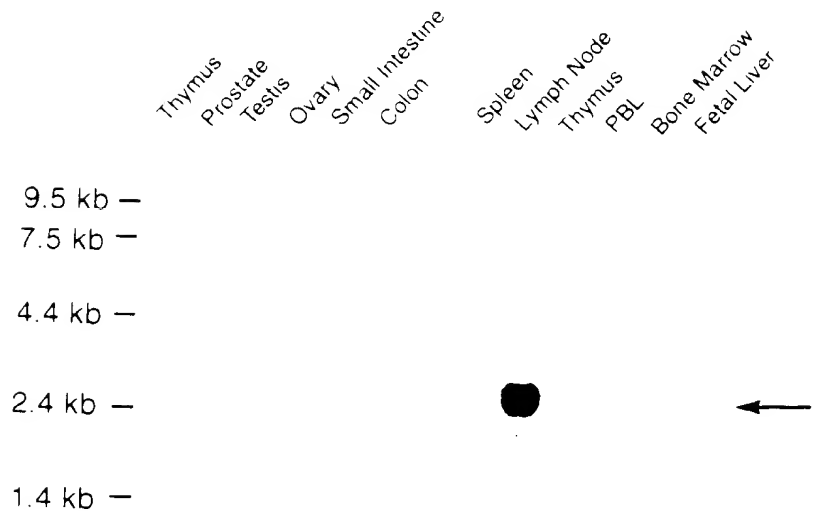


FIGURE 3

FIGURE 4

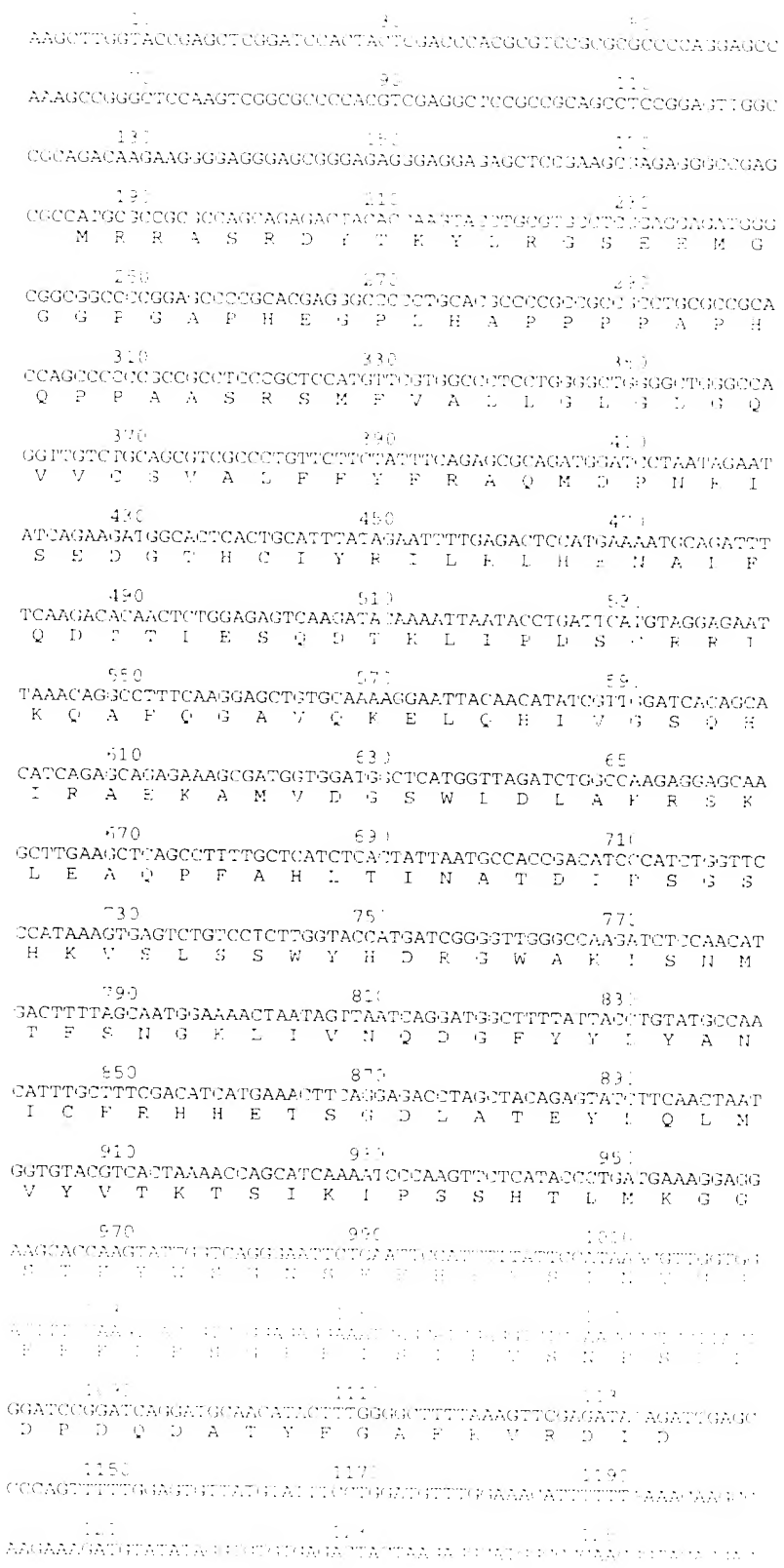


FIGURE 4 (Con't)

1390 1410 1430
CCAGATTGGAGCAATTACGGC TTGACCTTATGAGAAACTGCATGTGGGCTATGGGAGGGG

1450 1470 1490
TTGGTCCCTGGTCATGTGCCCCTTCGCAGCTGAAGTGGAGAGGGTGTCATCTAGCGCAAT

1510 1530 1550
TGAAGGATCATCTGAAGGGGCAAATTCTTTTGAATTGTTACATCATGCTGGAACCTGCAA

1570 1590 1610
AAAATACTTTTTCTAATGAGGAGAGAAAATATATGTATTTTTATATAATATCTAAAGTTA

1630 1650 1670
TATTTCAGATGTAATGTTTTCTTTGCAAAGTATTGTAAATTATATTTGTGCTATAGTATT

1690 1710 1730
TGATTCAAAATATTTAAAAATGTCTTGCTGTTGACATATTTAATGTTTTAAATGTACAGA

1750 1770 1790
CATATTTAACTGGTGCACTTTGTAAATTCCCTGGGGAAAACTTGCAGCTAAGGAGGGGAA

1810 1830 1850
AAAAATGTTGTTTCCTAATATCAAATGCAGTATATTTCTTCGTTCTTTTTAAGTTAATAG

1870 1890 1910
ATTTTTTGAGACTTGTCAAGCCTGTGCAAAAAAATTAAAATGGATGCCTTGAATAATAAG

1930 1950 1970
CAGGATGTTGGCCACCAGGTGCCTTTCAAATTTAGAAACTAATTGACTTTAGAAAGCTGA

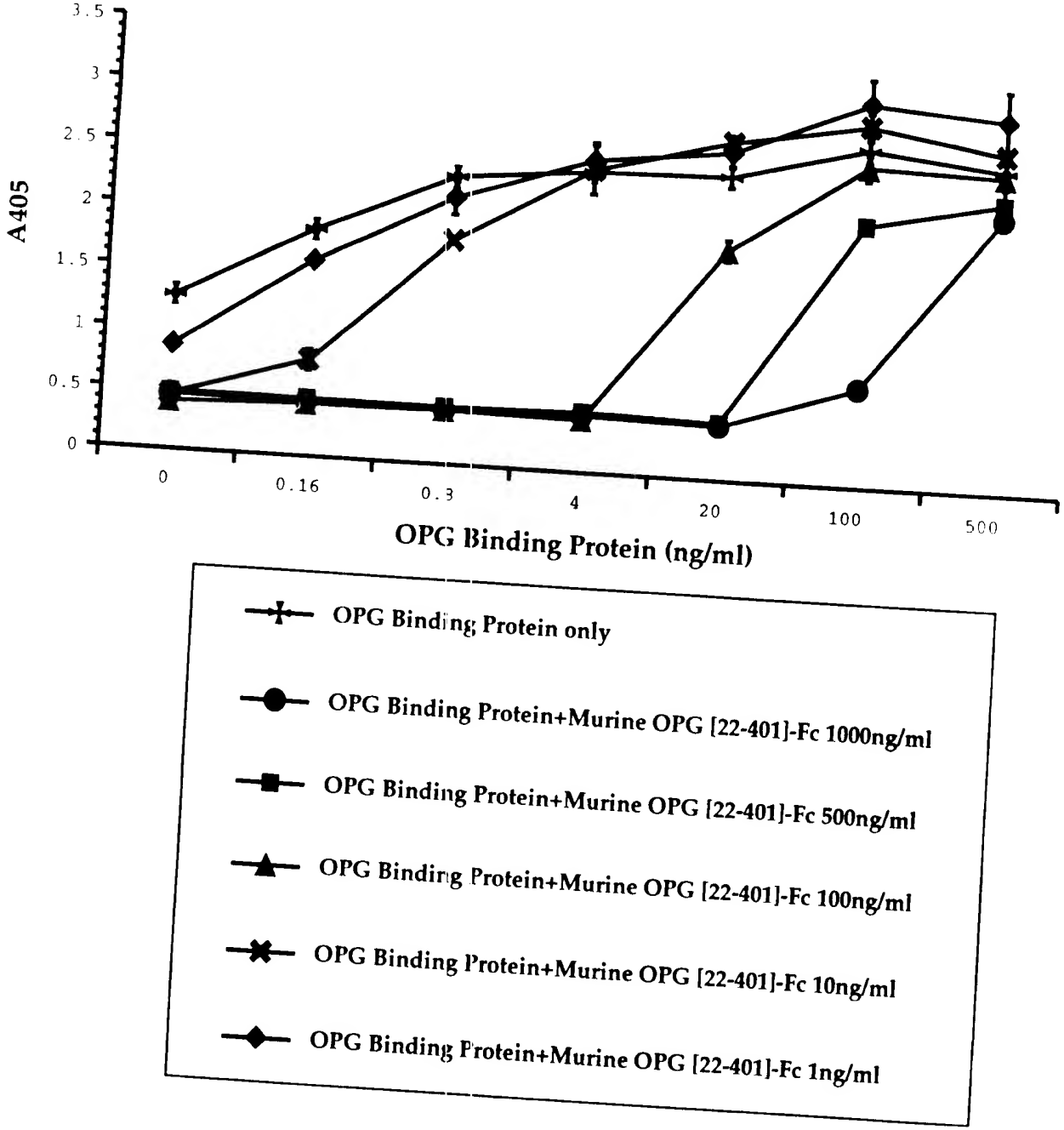
1990 2010 2030
CATTGCCAAAAAGGATACATAATGGGCCACTGAAATCTGTCAAGAGTAGTTATATAATTG

2050 2070 2090
TTCAAGAGGTGTTTTTTCCACAAGTGCCGCAAATTGTACCTTTTTTTTTTTTTTCAAAATAG

2110 2130 2150
AAAAGTTATTAGTGGTTTATCAGCAAAAAAGTCCAATTTTAATTTAGTAAATGTTATCTT

2170 2190 2210
ATACTGTACAATAAAAACATTGCCTTTGAATGTTAATTTTTTGGTACAAAAATAAATTTA

2230 2250 2270
TATGAAAAAAAAAAAAAAAAGGGCGGCCGCTCTAGAGGGCCCTATTCTATAG


A405
3.5
3
2.5
2
1.5
1
0.5
0
0
0.16
0.3
4
20
100
500
OPG Binding Protein (ng/ml)
OPG Binding Protein only
OPG Binding Protein+Murine OPG [22-401]-Fc 1000ng/ml
OPG Binding Protein+Murine OPG [22-401]-Fc 500ng/ml
OPG Binding Protein+Murine OPG [22-401]-Fc 100ng/ml
OPG Binding Protein+Murine OPG [22-401]-Fc 10ng/ml
OPG Binding Protein+Murine OPG [22-401]-Fc 1ng/ml

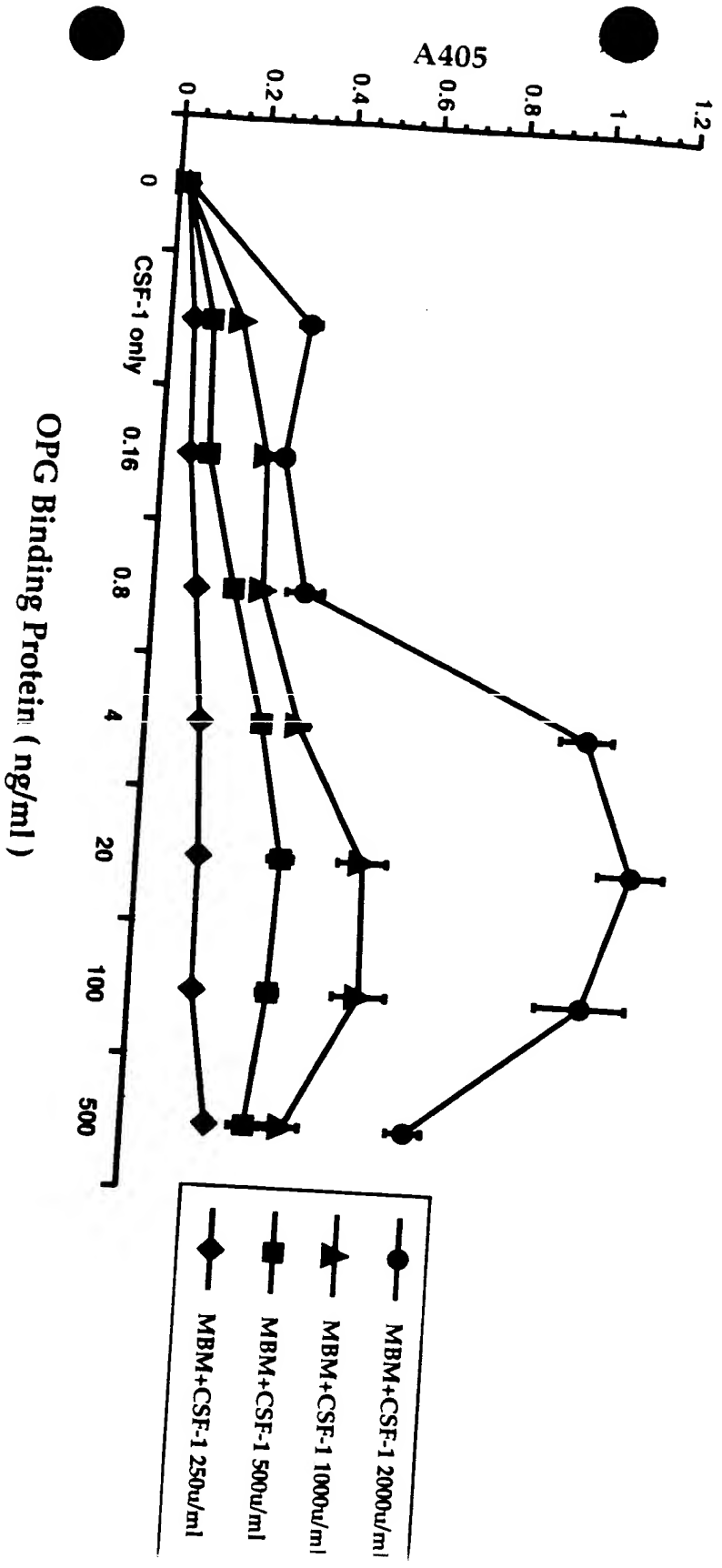
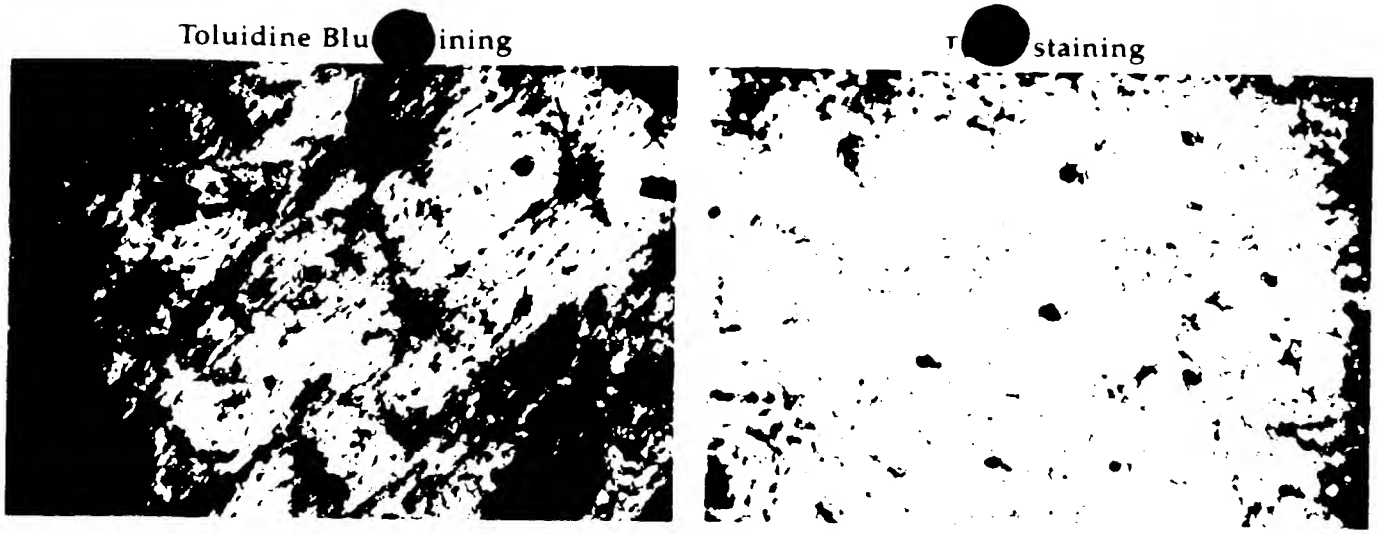
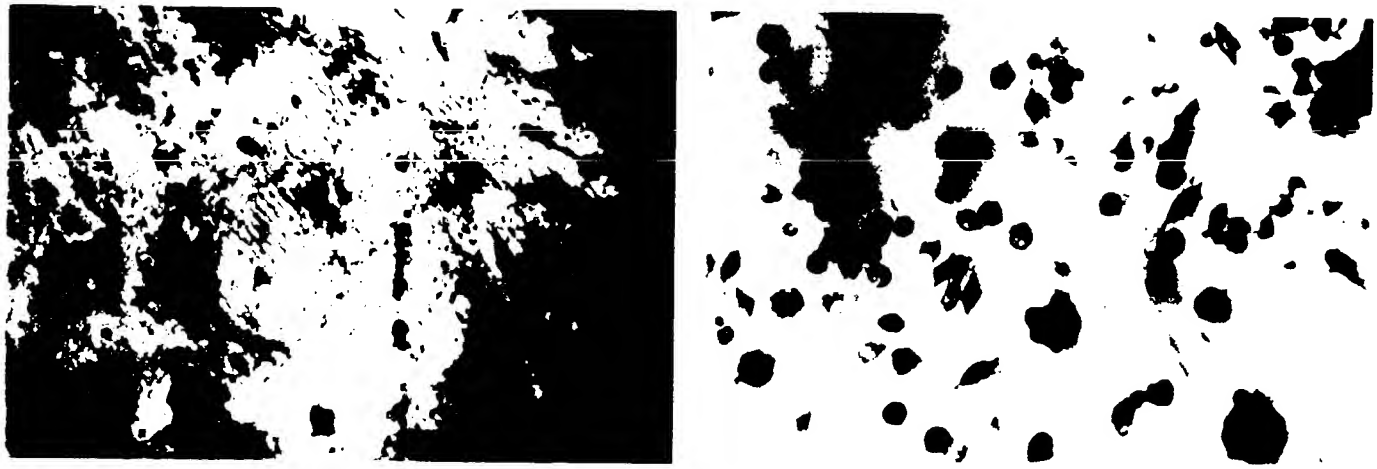

A405
0
0.2
0.4
0.6
0.8
1
1.2
OPG Binding Protein (ng/ml)
CSF-1 only
0.16
0.8
4
20
100
500
MBM+CSF-1 2000u/ml
MBM+CSF-1 1000u/ml
MBM+CSF-1 500u/ml
MBM+CSF-1 250u/ml

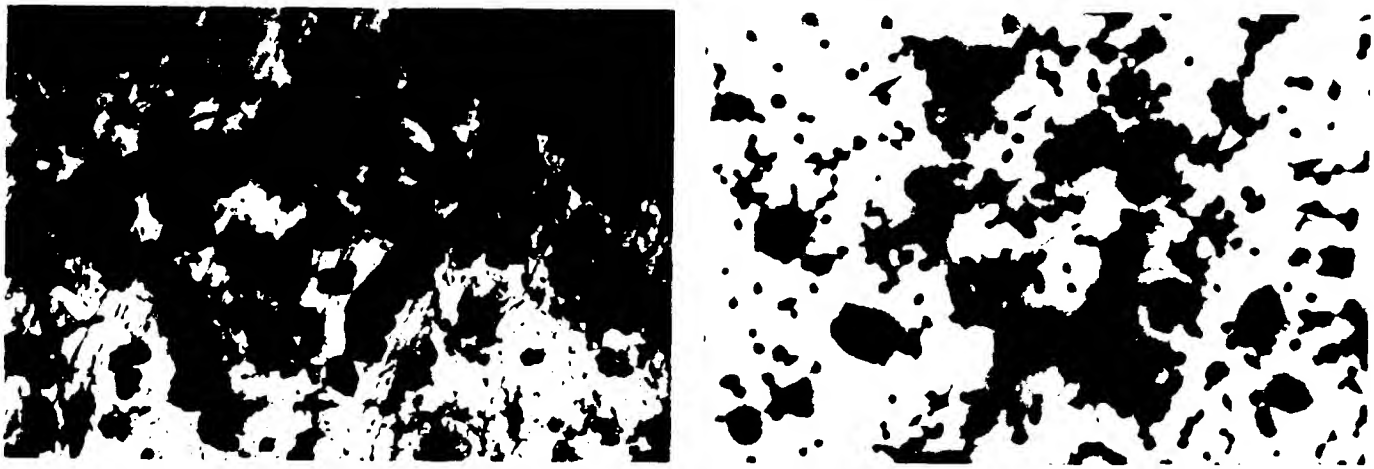
FIGURE 6



Bone Marrow Cells + M-CSF-1



Bone Marrow Cells + OPG Binding Protein



Bone Marrow Cells + M-CSF-1 +OPG Binding Protein

FIGURE

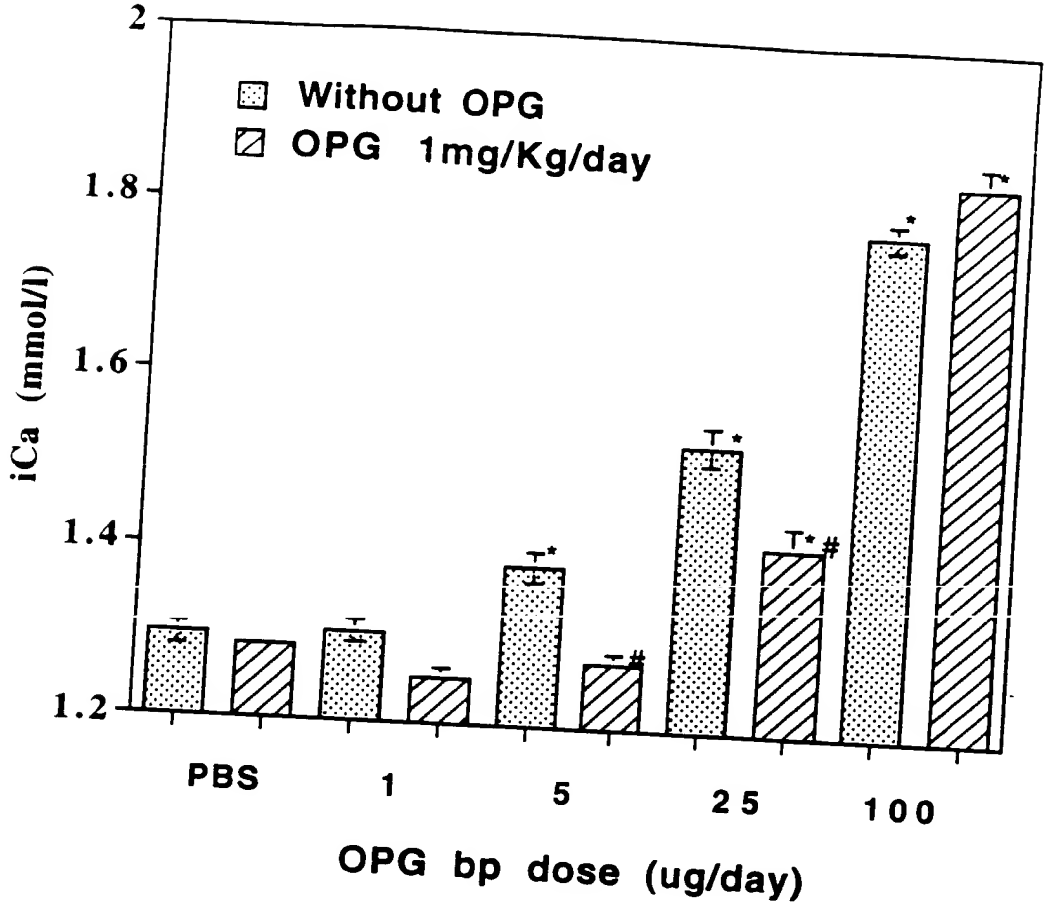

2
1.8
1.6
1.4
1.2
iCa (mmol/l)
Without OPG
OPG 1mg/Kg/day
PBS
1
5
25
100
OPG bp dose (ug/day)

FIGURE 8

PBS

OPGbp 5ug/d

OPGbp 25ug/d

OPGbp100ug/d

Figure 10. Murine ODAR cDNA sequence

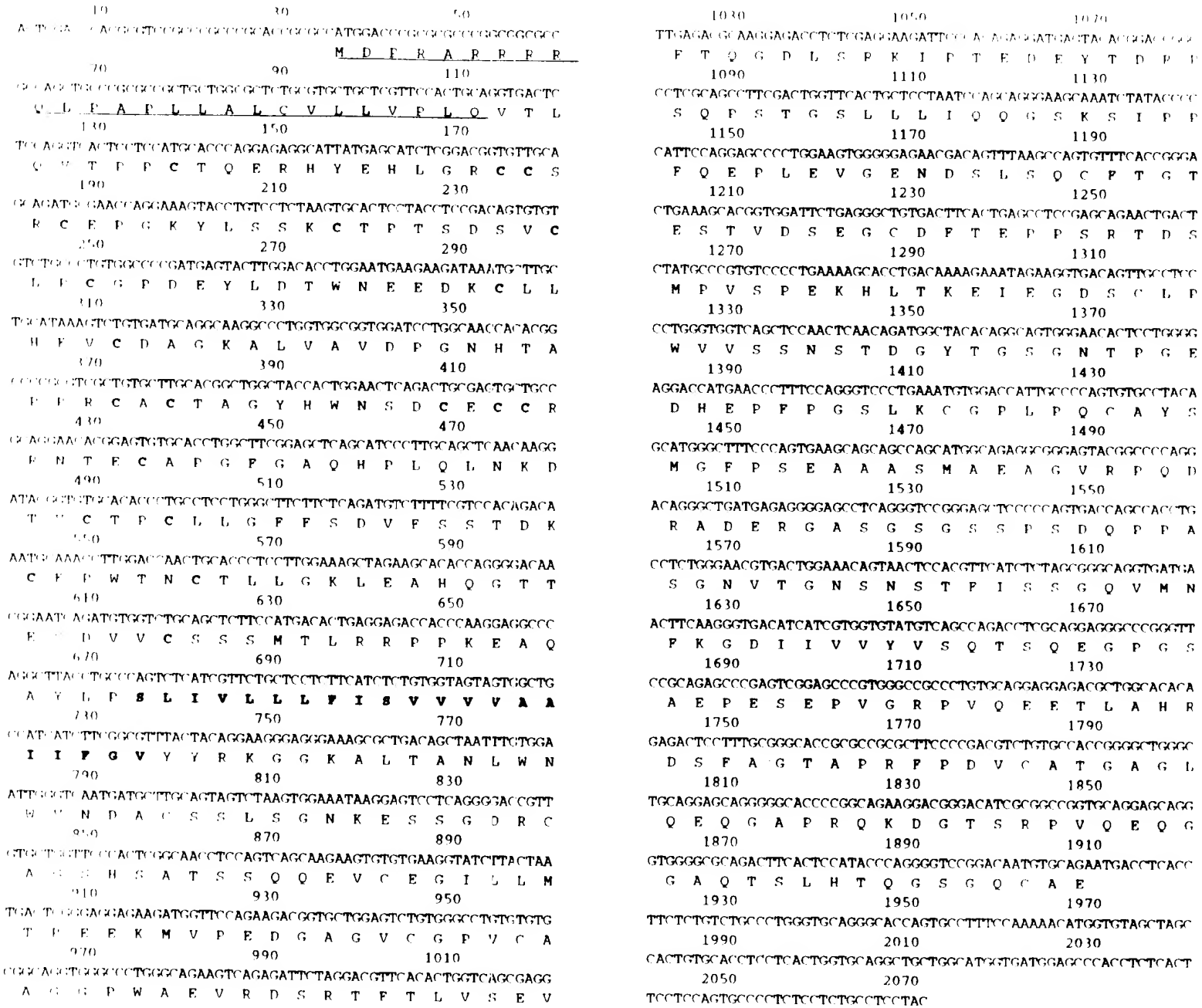


FIGURE 10

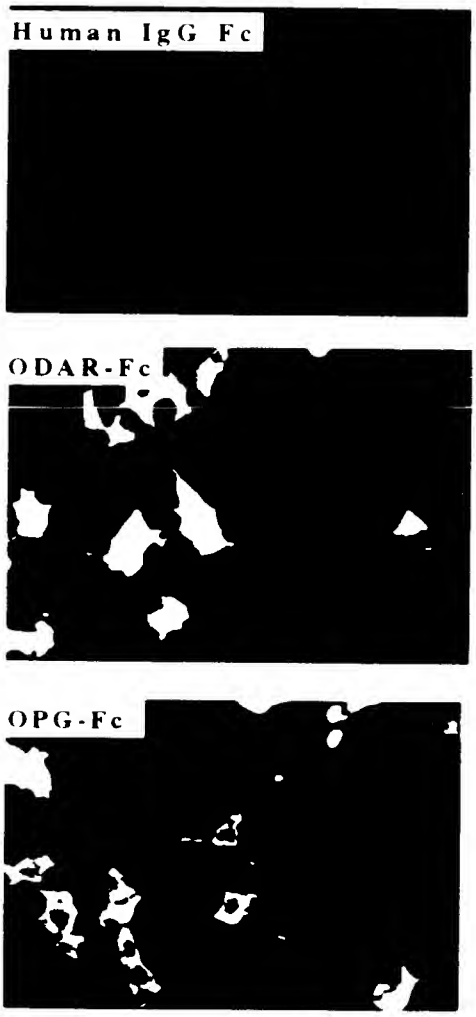
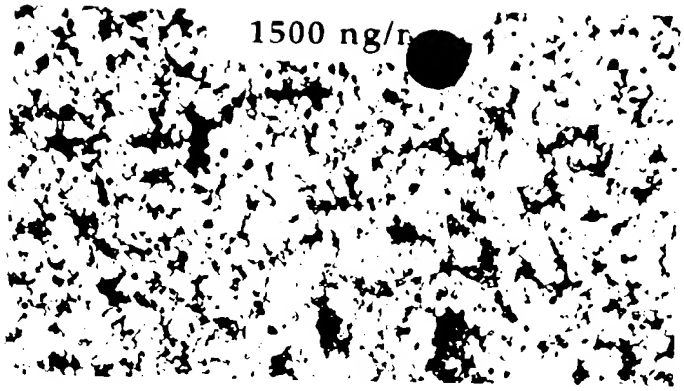
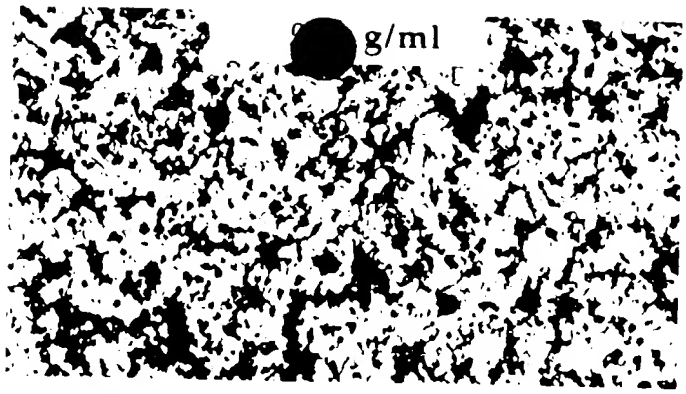
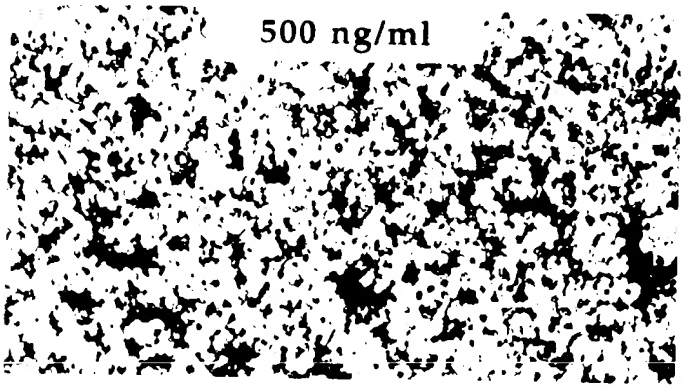
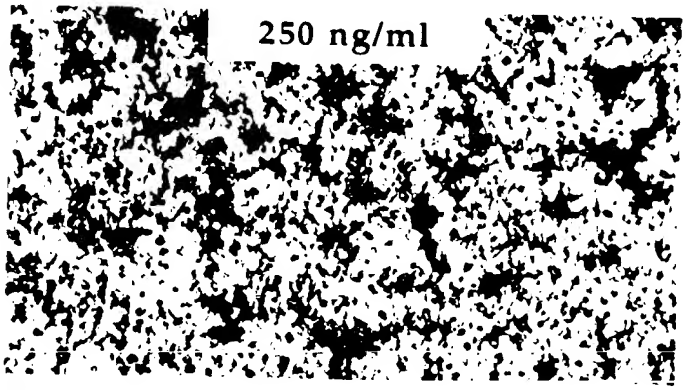


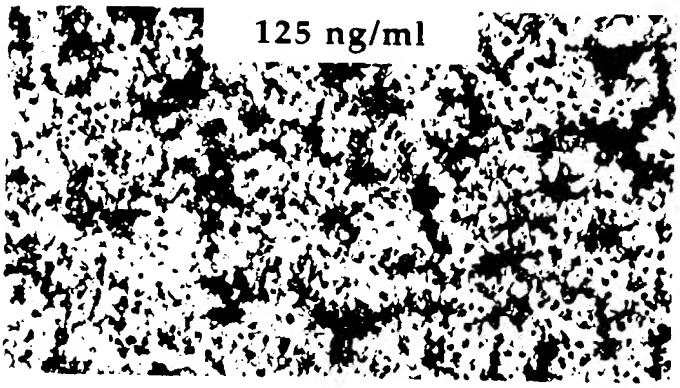
FIGURE 11

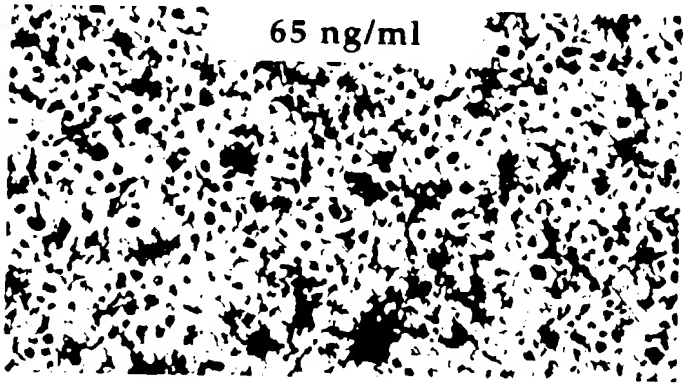

1500 ng/m

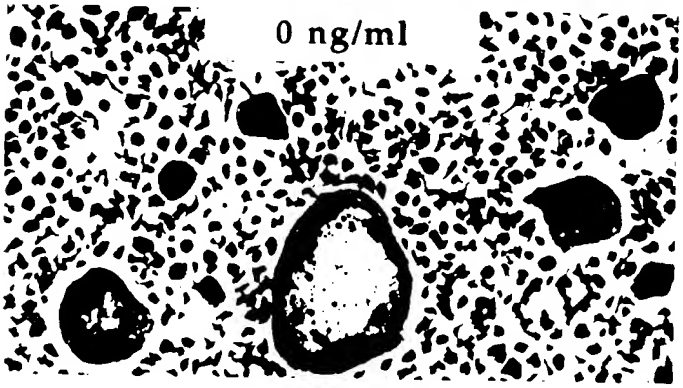

g/ml

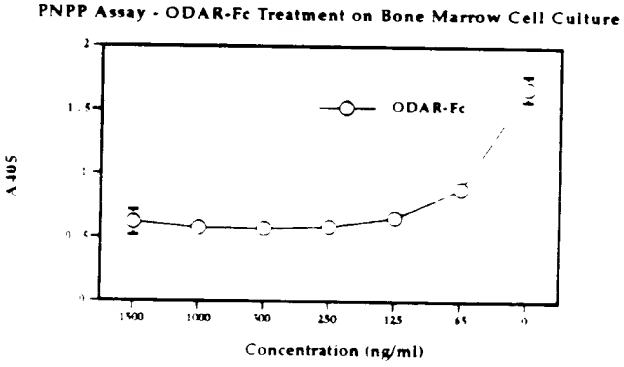

500 ng/ml


250 ng/ml


125 ng/ml

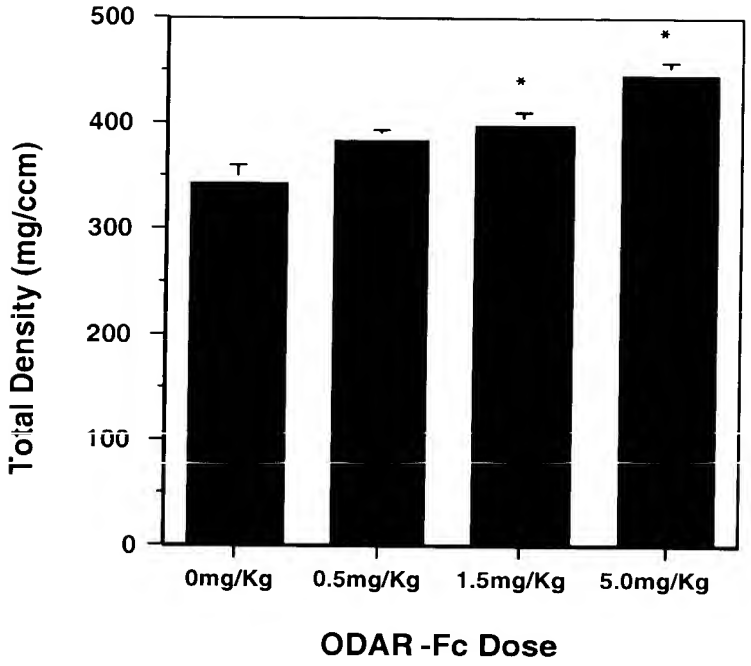

65 ng/ml


0 ng/ml


PNPP Assay - ODAR-Fc Treatment on Bone Marrow Cell Culture
ODAR-Fc
A 405
1500
1000
500
250
125
65
0
Concentration (ng/ml)

FIGURE

FIGURE 13



* Different to vehicle treated control $p < 0.05$.